

1 / 7 2

SEQUENCE LISTING

<110> Eisai Co., Ltd.

National Institute of Advanced Industrial Science and Technology

<120> METHOD OF SCREENING FOR COMPOUNDS THAT INHIBIT THE ENZYMATIC  
ACTIVITY OF GWT1 GENE PRODUCT

<130> E1-A0209P

<150> JP 2002-339418

<151> 2002-11-22

<160> 18

<170> PatentIn Ver. 2.0

<210> 1

<211> 1497

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1).. (1494)

&lt;400&gt; 1

atg gca aca gta cat cag aag aat atg tcg act tta aaa cag aga aaa 48

Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys

1

5

10

15

gag gac ttt gtg aca ggg ctc aat ggc ggt tct ata aca gaa att aac 96

Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn

20

25

30

gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg 144

Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu

35

40

45

aaa aat tcc aac ctt atg cct cct ggc att tcc agc gtg caa tac ata 192

Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile

50

55

60

att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att 240

Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile

65

70

75

80

tat gct agt gaa cca tac ctt cta aac acg cta ata ctg tta cct tgt 288

Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys

85

90

95

ttg ctc gca ttc ata tat gga aaa ttt act agc tcg agt aaa cct tct 336

Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser

100

105

110

aat cca ata tac aat aaa aaa aaa atg att aca cag cgg ttc caa cta 384

Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu

115

120

125

gaa aaa aag ccg tat att act gcg tat cgt ggt ggg atg ctt att ctg 432

Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu

130

135

140

act gct att gcc atc ttg gct gta gat ttt cca att ttc cca agg agg 480

Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg

145

150

155

160

ttt gcc aag gtg gaa act tgg ggg aca tcc ctg atg gat ctt ggt gta 528

Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val

165

170

175

gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg 576

Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu

180

185

190

aaa aac cta agc ttg aag agt aaa ccc agc ttc tta aaa aat gca ttt 624

Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe

195

200

205

aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg 672

Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg

210

215

220

ttg ttt ttt gta aaa aat ttg gaa tat caa gaa cat gtc aca gaa tat 720

Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr

225

230

235

240

ggg gtt cat tgg aat ttt ttt atc acc cta tca ttg ttg cca ctt gta 768

Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val

245

250

255

ttg acc ttt att gat ccc gtc aca aga atg gtt cca cgc tgc tca att 816

Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile

260

265

270

gca ata ttc att tca tgc att tat gaa tgg cta ctt tta aag gac gat 864

Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp

275

280

285

cgc act tta aac ttt tta att ttg gct gat aga aat tgt ttc ttc agt 912

Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser

290

295

300

gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt 960

5 / 7 2

Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe

305 310 315 320

ctt tgg ggc caa aac acg gga ttt tac ttg ttg gga aat aaa cca act 1008

Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr

325 330 335

tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca 1056

Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser

340 345 350

aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt 1104

Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser

355 360 365

ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt 1152

Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val

370 375 380

ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca 1200

Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro

385 390 395 400

tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac 1248

Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr

405 410 415

tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt 1296

Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val

420

425

430

gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg 1344

Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu

435

440

445

ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata 1392

Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile

450

455

460

gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca 1440

Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser

465

470

475

480

ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att 1488

Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile

485

490

495

aag cta taa

1497

Lys Leu

&lt;210&gt; 2

&lt;211&gt; 498

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 2

Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys

1

5

10

15

Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn

20

25

30

Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu

35

40

45

Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile

50

55

60

Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile

65

70

75

80

Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys

85

90

95

Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser

100

105

110

Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu

115

120

125

Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu

130

135

140

Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg

145

150

155

160

Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val

165

170

175

Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu

180

185

190

Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe

195

200

205

Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg

210

215

220

Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr

225

230

235

240

Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val



9 / 7 2

245

250

255

Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile

260

265

270

Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp

275

280

285

Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser

290

295

300

Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe

305

310

315

320

Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr

325

330

335

Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser

340

345

350

Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser

355

360

365

Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val

370

375

380

1 0 / 7 2

Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro

385 390 395 400

Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr

405 410 415

Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val

420 425 430

Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu

435 440 445

Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile

450 455 460

Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser

465 470 475 480

Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile

485 490 495

Lys Leu

&lt;211&gt; 1458

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1455)

&lt;400&gt; 3

atg tca tcg tct tta aaa caa ttg aaa gaa caa ttt gtc tca gat ttg 48

Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu

1

5

10

15

act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta 96

Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu

20

25

30

tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144

Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu

35

40

45

gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser

50

55

60

att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240

1 2 / 7 2

Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val

65 70 75 80

att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288

Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro

85 90 95

tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa 336

Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu

100 105 110

cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg 384

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu

115 120 125

ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca 432

Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro

130 135 140

aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta 480

Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu

145 150 155 160

gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa 528

Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln

165 170 175

ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat 576

Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr

180

185

190

ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt 624

Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val

195

200

205

tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa 672

Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu

210

215

220

cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg 720

His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly

225

230

235

240

ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt 768

Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val

245

250

255

cca cgc ttc ata ata gga att ggt atc tca att gct tat gag gta gcg 816

Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala

260

265

270

ttg aat aag act ggt ttg ttg aag ttc att ttg agc agc gaa aac aga 864

1 4 / 7 2

Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg

275

280

285

ctt gaa tct ctc atc acc atg aat aaa gaa ggt att ttt tcg ttt att 912

Leu Glu Ser Leu Ile Thr Met Asn Lys Glu Gly Ile Phe Ser Phe Ile

290

295

300

gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt 960

Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val

305

310

315

320

tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att 1008

Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile

325

330

335

cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca 1056

Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser

340

345

350

gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta 1104

Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu

355

360

365

gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca 1152

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser

370

375

380

aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat 1200

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn

385

390

395

400

gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg 1248

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly

405

410

415

aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt 1296

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe

420

425

430

atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc 1344

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc 1392

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly

450

455

460

tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag 1440

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys

465

470

475

480

atc tac atc aag ctt tag

1458

Ile Tyr Ile Lys Leu

485

<210> 4

<211> 485

<212> PRT

<213> Candida albicans

<400> 4

Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu

1

5

10

15

Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu

20

25

30

Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu

35

40

45

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser

50

55

60

Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val

65

70

75

80

Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro



1 7 / 7 2

85

90

95

Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu

100

105

110

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu

115

120

125

Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro

130

135

140

Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu

145

150

155

160

Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln

165

170

175

Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr

180

185

190

Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val

195

200

205

Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu

210

215

220

1 8 / 7 2

His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly

225 230 235 240

Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val

245 250 255

Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala

260 265 270

Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg

275 280 285

Leu Glu Ser Leu Ile Thr Met Asn Lys Glu Gly Ile Phe Ser Phe Ile

290 295 300

Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val

305 310 315 320

Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile

325 330 335

Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser

340 345 350

Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu

355 360 365

19 / 72

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser

370

375

380

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn

385

390

395

400

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly

405

410

415

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe

420

425

430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly

450

455

460

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys

465

470

475

480

Ile Tyr Ile Lys Leu

485

20 / 72

<210> 5

<211> 1458

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1455)

<400> 5

atg tca tcg tct tta aaa caa ttg aaa gaa caa ttt gtc tca gat ttg 48

Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu

1

5

10

15

act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta 96

Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu

20

25

30

tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144

Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu

35

40

45

gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser

50

55

60

att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240  
 Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val  
 65 70 75 80

att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288  
 Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro  
 85 90 95

tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa 336  
 Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu  
 100 105 110

cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg 384  
 Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu  
 115 120 125

ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca 432  
 Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro  
 130 135 140

aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta 480  
 Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu  
 145 150 155 160

gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa 528  
 Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln

2 2 / 7 2

165

170

175

ttg atc aag aac cac acc gac aat tac aaa ttt agt tgg aag agt tat 576

Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr

180

185

190

ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt 624

Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val

195

200

205

tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa 672

Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu

210

215

220

cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg 720

His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly

225

230

235

240

ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt 768

Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val

245

250

255

cca cgc ttc ata ata gga att ggt atc tca att ggt tat gag gta gcg 816

Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala

260

265

270

23/72

ttg aat aag act ggt ttg ttg aag ttc att ttg agc agc gaa aac aga 864

Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg

275

280

285

ctt gaa tct ctc atc gcc atg aat aaa gaa ggt att ttt tcg ttt att 912

Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile

290

295

300

gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt 960

Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val

305

310

315

320

tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att 1008

Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile

325

330

335

cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca 1056

Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser

340

345

350

gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta 1104

Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu

355

360

365

gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca 1152

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser

370

375

380

aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat 1200

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn

385

390

395

400

gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg 1248

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly

405

410

415

aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt 1296

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe

420

425

430

atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc 1344

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc 1392

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly

450

455

460

tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag 1440

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys

465

470

475

480



2 5 / 7 2

atc tac atc aag ctt tag

1458

Ile Tyr Ile Lys Leu

485

<210> 6

<211> 485

<212> PRT

<213> Candida albicans

<400> 6

Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu

1

5

10

15

Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu

20

25

30

Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu

35

40

45

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser

50

55

60

Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val

65

70

75

80

26 / 72

Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro

85

90

95

Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu

100

105

110

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu

115

120

125

Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro

130

135

140

Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu

145

150

155

160

Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln

165

170

175

Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr

180

185

190

Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val

195

200

205

Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu

210

215

220

27/72

His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly

225 230 235 240

Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val

245 250 255

Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala

260 265 270

Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg

275 280 285

Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile

290 295 300

Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val

305 310 315 320

Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile

325 330 335

Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser

340 345 350

Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu

28 / 72

355

360

365

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser

370

375

380

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn

385

390

395

400

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly

405

410

415

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe

420

425

430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly

450

455

460

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys

465

470

475

480

Ile Tyr Ile Lys Leu

485

&lt;210&gt; 7

&lt;211&gt; 1380

&lt;212&gt; DNA

&lt;213&gt; Schizosaccharomyces pombe

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1380)

&lt;400&gt; 7

atg tca tac aaa ttg gaa aaa gaa gca ttt gtc tca aac ctg acg ggt 48

Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly

1

5

10

15

tca agt tcc att gag aca tgt ggc ttg tta tta ata gga att gct tgc 96

Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys

20

25

30

aac gtt ttg tgg gta aac atg act gcg aga aac atc tta ccc aaa ggg 144

Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly

35

40

45

aat ctt ggg ttt ctt gtt gag ttt ttc atc ttt tgc tta att cca tta 192

Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu

50

55

60

ttt gtc att tac gtt tca tgc aaa gtt ggc gtt ttc act ctt tgc ata 240  
 Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile  
 65 70 75 80

gcc tct ttt ttg cct tcc ttc gtc ctt cat gtt ata agt cca att aat 288  
 Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn  
 85 90 95

tgg gat gtg ctg aga aga aaa cct ggt tgt tgt ctt act aaa aaa aat 336  
 Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn  
 100 105 110

gaa aat act ttt gat cga cga att gct gga gtc aca ttt tat cgt tct 384  
 Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser  
 115 120 125

caa atg atg ttg gtt act gtc act tgc atc ctg gcc gtt gac ttt acc 432  
 Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr  
 130 135 140

ctt ttc ccg agg aga tat gcc aaa gtt gaa acc tgg gga aca tca ctg 480  
 Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu  
 145 150 155 160

atg gat ctt ggt gtt gga tct ttc atg ttt tct tca ggt act gtg gct 528

3 1 / 7 2

Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala

165

170

175

gga cgg aaa aat gac att aaa aaa cca aat gcg ttt aaa aat gta ttg 576

Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu

180

185

190

tgg aat tct ttc atc ctt ttg att tta gga ttt gcg cgc atg ttt tta 624

Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu

195

200

205

acg aaa agc atc aat tac caa gaa cat gta agc gaa tat ggc atg cat 672

Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His

210

215

220

tgg aac ttt ttt ttc acc cta ggt ttc atg gct ctt ggc gta ttt ttt 720

Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe

225

230

235

240

ttt cgt cgt tct tta aaa aaa gtc tcc tat ttt aat tta gca acc ttc 768

Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe

245

250

255

att act ctt ctt cat cat tgt ttg ctt gtt tta acc cct ttc caa aaa 816

Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys

260

265

270

tgg gca cta tcc gcc ccc aga aca aat att ttg gct cag aat aga gag 864

Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu

275

280

285

ggg att gct tct ctt ccc gga tac att gct att tac ttt tat gga atg 912

Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met

290

295

300

tat acc ggt agt gta gtt ttg gct gat cga cct cta atg tat act aga 960

Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg

305

310

315

320

gct gag tcg tgg aag cgc ttt caa cgt cta tta ttc ccg cta tgc att 1008

Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile

325

330

335

ttg tta gtg ttg tat ctt gtg tct aac ttt ttg tca gtt ggt gtt tct 1056

Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser

340

345

350

cgc cga ctt gct aat acg cct tat gtt gcg aat gtt gcc ttt atc aat 1104

Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn

355

360

365

atg ttt ttt ctt act ata tac ata ctt att gat gcc tat tta ttc cca 1152



3 3 / 7 2

Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro

370

375

380

tct tct gtg cca tat gga agt cgc gtc ccc aaa ctg ctt gaa gat gcc 1200

Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala

385

390

395

400

aat aat aat ggc ttg ttg gtg ttt ttg att gct aac gtt tta aca gga 1248

Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly

405

410

415

gta gtt aat tta tcg ttc gac acc ctt cat tct agc aat gca aaa ggc 1296

Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly

420

425

430

ttg aca atc atg act atg tat ctt ttt att att tgc tat atg gca cat 1344

Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His

435

440

445

tgg ctt gct caa cac gga att cgt ttt cgc ctt tag 1380

Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu

450

455

460

<210> 8

<211> 459

3 4 / 7 2

<212> PRT

<213> Schizosaccharomyces pombe

<400> 8

Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly

1 5 10 15

Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys

20 25 30

Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly

35 40 45

Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu

50 55 60

Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile

65 70 75 80

Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn

85 90 95

Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn

100 105 110

Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser

3 5 / 7 2

115

120

125

Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr

130

135

140

Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu

145

150

155

160

Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala

165

170

175

Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu

180

185

190

Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu

195

200

205

Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His

210

215

220

Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe

225

230

235

240

Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe

245

250

255

3 6 / 7 2

Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys

260

265

270

Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu

275

280

285

Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met

290

295

300

Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg

305

310

315

320

Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile

325

330

335

Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser

340

345

350

Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn

355

360

365

Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro

370

375

380

Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala

385

390

395

400

37/72

Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly

405

410

415

Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly

420

425

430

Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His

435

440

445

Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu

450

455

<210> 9

<211> 1576

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<221> CDS

<222> (31)..(1536)

<400> 9

aaggtgcaaa tcccgcggca ttgagtcaag atg gat cca gat tat aaa gct cgc 54

Met Asp Pro Asp Tyr Lys Ala Arg

38 / 72

1

5

aaa gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc 102

Lys Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile

10

15

20

aac gcc gtc acc ttg gtt gct tcg gta tcc gtt ttt ctg tgg tca att 150

Asn Ala Val Thr Leu Val Ala Ser Val Ser Val Phe Leu Trp Ser Ile

25

30

35

40

cta caa tct cgc cta tcc ttt ttc aca ccc tac agc gcc gct gcc ctt 198

Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr Ser Ala Ala Ala Leu

45

50

55

ctc gtt gat ttc ctg ctc aat gta cta gct atc ttg ttc gca acc act 246

Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile Leu Phe Ala Thr Thr

60

65

70

tta tac tct tcg gcg cct ctt ctt ctc aat ctc ctt cta ata tct ccc 294

Leu Tyr Ser Ser Ala Pro Leu Leu Leu Asn Leu Leu Leu Ile Ser Pro

75

80

85

gct ctg ctg ata ctc ctc tct acg aaa cgt cct cgg acc ccc gtc aaa 342

Ala Leu Leu Ile Leu Leu Ser Thr Lys Arg Pro Arg Thr Pro Val Lys

90

95

100

gcg aaa cct cct cgc cag tcc gct aga gct ggg aaa gat gac tcg aaa 390

Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly Lys Asp Asp Ser Lys

105 110 115 120

cat gcg aca gcc ttg cca gag tct cta ccc att cat cca ttt ctc acg 438

His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile His Pro Phe Leu Thr

125 130 135

aca tat cgc gcc gcc atg atg gtt atc acg tgc atc gct atc ttg gct 486

Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys Ile Ala Ile Leu Ala

140 145 150

gtg gat ttt cgc att ttt cct cgc cga ttc gcc aag gta gaa aac tgg 534

Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala Lys Val Glu Asn Trp

155 160 165

ggt aca tca ctc atg gat ctg ggc gtt gga tcg ttt gtc ttt tcg ggc 582

Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser Phe Val Phe Ser Gly

170 175 180

gga gta gta tcc gct cgc tca cta ctc aag agc agg acc aat ggc tct 630

Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser Arg Thr Asn Gly Ser

185 190 195 200

aaa agg ttg cct ctt gcc aag agg ttg att gcg tcg acg cga cac tct 678

Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala Ser Thr Arg His Ser

205	210	215	
att cct ctg ctc gtc ctc ggc ctg att cgg cta tac agc gtc aaa ggc			726
Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu Tyr Ser Val Lys Gly			
220	225	230	
ttg gac tat gcg gag cac gtc acc gag tac ggc gta cat tgg aac ttc			774
Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe			
235	240	245	
ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg gag gtc ttc gac gcc			822
Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val Glu Val Phe Asp Ala			
250	255	260	
ttg gct acg atc att ccg tca tac gag gtt ctc tcc gtg ggg atc gcc			870
Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu Ser Val Gly Ile Ala			
265	270	275	280
gtc ttg tat caa gtt gcc cta gag tca aca gac ttg aaa agc tac atc			918
Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp Leu Lys Ser Tyr Ile			
285	290	295	
ctc gtc tcc cct cgt ggg cca agc tta ctg tcc aag aat cgt gaa ggc			966
Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser Lys Asn Arg Glu Gly			
300	305	310	



gtc ttc tcc ttc tca ggt tat ctc gcg att ttt ctt gct ggt cgt gcg 1014

Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe Leu Ala Gly Arg Ala

315

320

325

atc ggc att cgg ata atc cct cgc gga act tct ttc tca aga agc cca 1062

Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser Phe Ser Arg Ser Pro

330

335

340

gaa cag gcc agg aga cgg gtc ctg atc agc ctt ggc gtg caa gcg tta 1110

Glu Gln Ala Arg Arg Arg Val Leu Ile Ser Leu Gly Val Gln Ala Leu

345

350

355

360

gtg tgg acc act ctt ttt gtg ttg aac tcc act tat gcg atg gga tac 1158

Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr Tyr Ala Met Gly Tyr

365

370

375

gga gct aat atc cct gtc tcc cgc cgc ctc gct aac atg ccc tat gtc 1206

Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala Asn Met Pro Tyr Val

380

385

390

ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg ttt gtg ttc tgc ctg 1254

Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu Phe Val Phe Cys Leu

395

400

405

atc gaa aca ctc tgc ttt cct gca gtt cat cgg aca acg act caa gag 1302

Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg Thr Thr Thr Gln Glu

4 2 / 7 2

410	415	420	
agc gaa tct gag cga gtc gat ttt gct acg agc cga atc atg tcg gcc 1350			
Ser Glu Ser Glu Arg Val Asp Phe Ala Thr Ser Arg Ile Met Ser Ala			
425	430	435	440
ttc aat aag aac agt ctc gcg atc ttt ctt ttg gcc aat ctt ctg act 1398			
Phe Asn Lys Asn Ser Leu Ala Ile Phe Leu Leu Ala Asn Leu Leu Thr			
445	450	455	
gga gct gtg aat ctg agc atc tcc aca att gat gct aat aca gcg cag 1446			
Gly Ala Val Asn Leu Ser Ile Ser Thr Ile Asp Ala Asn Thr Ala Gln			
460	465	470	
gcc atc gct gtt ctc att gga tat tca tcc att atc aca ggg gtt gct 1494			
Ala Ile Ala Val Leu Ile Gly Tyr Ser Ser Ile Ile Thr Gly Val Ala			
475	480	485	
cta gca ttg cat cat gcc aat atc aaa gta ctt cct ttc tag 1536			
Leu Ala Leu His His Ala Asn Ile Lys Val Leu Pro Phe			
490	495	500	
ggtattttacg agcaattggt ggtgtgttga agatatatag 1576			

4 3 / 7 2

<211> 501

<212> PRT

<213> *Aspergillus fumigatus*

<400> 10

Met Asp Pro Asp Tyr Lys Ala Arg Lys Glu Ala Phe Val Ser Gly Leu

1

5

10

15

Ala Gly Gly Ser Ile Leu Glu Ile Asn Ala Val Thr Leu Val Ala Ser

20

25

30

Val Ser Val Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe

35

40

45

Thr Pro Tyr Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val

50

55

60

Leu Ala Ile Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu

65

70

75

80

Leu Asn Leu Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr

85

90

95

Lys Arg Pro Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala

100

105

110

44 / 72

Arg Ala Gly Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser

115

120

125

Leu Pro Ile His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val

130

135

140

Ile Thr Cys Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg

145

150

155

160

Arg Phe Ala Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly

165

170

175

Val Gly Ser Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu

180

185

190

Leu Lys Ser Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg

195

200

205

Leu Ile Ala Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu

210

215

220

Ile Arg Leu Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr

225

230

235

240

Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro

245

250

255

4 5 / 7 2

Pro Phe Val Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr

260

265

270

Glu Val Leu Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu

275

280

285

Ser Thr Asp Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser

290

295

300

Leu Leu Ser Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu

305

310

315

320

Ala Ile Phe Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg

325

330

335

Gly Thr Ser Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu

340

345

350

Ile Ser Leu Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu

355

360

365

Asn Ser Thr Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg

370

375

380

Arg Leu Ala Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr

4 6 / 7 2

385

390

395

400

Ala Gln Leu Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala

405

410

415

Val His Arg Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe

420

425

430

Ala Thr Ser Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile

435

440

445

Phe Leu Leu Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser

450

455

460

Thr Ile Asp Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr

465

470

475

480

Ser Ser Ile Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile

485

490

495

Lys Val Leu Pro Phe

500

<210> 11

<211> 1648

47/72

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<221> intron

<222> (122)..(198)

<220>

<221> CDS

<222> (26)..(121)

<220>

<221> CDS

<222> (199)..(1608)

<400> 11

gcaaatcccg cggcattgag tcaag atg gat cca gat tat aaa gct cgc aaa 52

Met Asp Pro Asp Tyr Lys Ala Arg Lys

1

5

gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc aac 100

Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile Asn

10

15

20

25

gcc gtc acc ttg gtt gct tcg gttcgtgtta ctatcttatt gtggctactt 151

Ala Val Thr Leu Val Ala Ser

cgcctacatt gtttctcgac taaccgagtc tctttgcat caatcag gta tcc gtt 207

Val Ser Val

35

ttt ctg tgg tca att cta caa tct cgc cta tcc ttt ttc aca ccc tac 255

Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr

40

45

50

agc gcc gct gcc ctt ctc gtt gat ttc ctg ctc aat gta cta gct atc 303

Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile

55

60

65

ttg ttc gca acc act tta tac tct tcg gcg cct ctt ctt ctc aat ctc 351

Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu Leu Asn Leu

70

75

80

ctt cta ata tct ccc gct ctg ctg ata ctc ctc tct acg aaa cgt cct 399

Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr Lys Arg Pro

85

90

95

cgg acc ccc gtc aaa gcg aaa cct cct cgc cag tcc gct aga gct ggg 447

Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly

100

105

110

115



aaa gat gac tcg aaa cat gcg aca gcc ttg cca gag tct cta ccc att 495

Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile

120

125

130

cat cca ttt ctc acg aca tat cgc gcc gcc atg atg gtt atc acg tgc 543

His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys

135

140

145

atc gct atc ttg gct gtg gat ttt cgc att ttt cct cgc cga ttc gcc 591

Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala

150

155

160

aag gta gaa aac tgg ggt aca tca ctc atg gat ctg ggc gtt gga tcg 639

Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser

165

170

175

ttt gtc ttt tcg ggc gga gta gta tcc gct cgc tca cta ctc aag agc 687

Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser

180

185

190

195

agg acc aat ggc tct aaa agg ttg cct ctt gcc aag agg ttg att gcg 735

Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala

200

205

210

tcg acg cga cac tct att cct ctg ctc gtc ctc ggc ctg att cgg cta 783

Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu

50 / 72

215

220

225

tac agc gtc aaa ggc ttg gac tat gcg gag cac gtc acc gag tac ggc 831

Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly

230

235

240

gta cat tgg aac ttc ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg 879

Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val

245

250

255

gag gtc ttc gac gcc ttg gct acg atc att ccg tca tac gag gtt ctc 927

Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu

260

265

270

275

tcc gtg ggg atc gcc gtc ttg tat caa gtt gcc cta gag tca aca gac 975

Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp

280

285

290

ttg aaa agc tac atc ctc gtc tcc cct cgt ggg cca agc tta ctg tcc 1023

Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser

295

300

305

aag aat cgt gaa ggc gtc ttc tcc ttc tca ggt tat ctc gcg att ttt 1071

Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe

310

315

320

ctt gct ggt cgt gcg atc ggc att cgg ata atc cct cgc gga act tct 1119

Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser

325

330

335

ttc tca aga agc cca gaa cag gcc agg aga cgg gtc ctg atc agc ctt 1167

Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu Ile Ser Leu

340

345

350

355

ggc gtg caa gcg tta gtg tgg acc act ctt ttt gtg ttg aac tcc act 1215

Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr

360

365

370

tat gcg atg gga tac gga gct aat atc cct gtc tcc cgc cgc ctc gct 1263

Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala

375

380

385

aac atg ccc tat gtc ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg 1311

Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu

390

395

400

ttt gtg ttc tgc ctg atc gaa aca ctc tgc ttt cct gca gtt cat cgg 1359

Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg

405

410

415

aca acg act caa gag agc gaa tct gag cga gtc gat ttt gct acg agc 1407

Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe Ala Thr Ser

5 2 / 7 2

420	425	430	435	
cga atc atg tcg gcc ttc aat aag aac agt ctc gcg atc ttt ctt ttg				1455
Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile Phe Leu Leu				
	440	445	450	
gcc aat ctt ctg act gga gct gtg aat ctg agc atc tcc aca att gat				1503
Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser Thr Ile Asp				
	455	460	465	
gct aat aca gcg cag gcc atc gct gtt ctc att gga tat tca tcc att				1551
Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr Ser Ser Ile				
	470	475	480	
atc aca ggg gtt gct cta gca ttg cat cat gcc aat atc aaa gta ctt				1599
Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile Lys Val Leu				
	485	490	495	
cct ttc tag ggtatttacg agcaattggt ggtgtgttga agatatatag				1648
Pro Phe				
500				

<210> 12

<211> 2045

<212> DNA

5 3 / 7 2

<213> Cryptococcus neoformans

<220>

<221> intron

<222> (137).. (198)

<220>

<221> intron

<222> (892).. (942)

<220>

<221> intron

<222> (1636).. (1686)

<220>

<221> CDS

<222> (44).. (2001)

<400> 12

gtcatagcat taaatccccg ccataataag ctactgaatt gca atg ggg gat tac 55

Met Gly Asp Tyr

1

aag tcg gcc aaa gag gcc ttt gtc tcg gat aac cca ggt gct tct atc 103

Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro Gly Ala Ser Ile

5

10

15

20

tgg agt atc aac gct gtc agc ctg gtc gca ctg gtagtagct cgttctccga 156

Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu

25

30

ggggttctgt catttggaga cgcttattaa ttgggatcgc ag gcg aca tat gct 210

Ala Thr Tyr Ala

35

ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac 258

Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn

40

45

50

tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc atc ttc tca 306

Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser

55

60

65

act tcg cct ctc gta ttt acc tct ttt ttg tcc att att tcc ctc gct 354

Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile Ser Leu Ala

70

75

80

ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt tcg ccc gaa 402

Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu

85

90

95

aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat gag gaa cca 450

5 5 / 7 2

Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp Glu Glu Pro

100 105 110 115

gcg gaa cct gct tct gca gct gga tct gca gca gtc tca cca gta aag 498

Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser Pro Val Lys

120 125 130

ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta tta tct ccc 546

Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu Leu Ser Pro

135 140 145

gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca gct tca gga 594

Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser Ala Ser Gly

150 155 160

cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg agg tcg cta 642

His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg Arg Ser Leu

165 170 175

tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac tcc aag gtc 690

Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp Ser Lys Val

180 185 190 195

aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct agg gca acg 738

Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser Arg Ala Thr

200 205 210

aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt ttg aca gtg 786

Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe Leu Thr Val

215

220

225

tac cga gcg cac atg atg ctc atg act gtt atc tgc atc ttg gcg gta 834

Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile Leu Ala Val

230

235

240

gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa gat ttt ggt 882

Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu Asp Phe Gly

245

250

255

act agt ctg gtaagctttc cttcagccat ggtccagtgc tcaccgctct 931

Thr Ser Leu

260

acttgccgta g atg gac gtg ggt gtc ggg tca ttc gtc ttt tcc ctc ggt 981

Met Asp Val Gly Val Gly Ser Phe Val Phe Ser Leu Gly

265

270

275

ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act cct acg ccc 1029

Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr Pro Thr Pro

280

285

290

tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc ccg tcc ccg 1077



57/72

Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr Pro Ser Pro

295

300

305

ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc atc ctc gtc 1125

Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro Ile Leu Val

310

315

320

ctc ggc ttt ata cgg ttg att atg gtc aag gga tct gat tat cct gag 1173

Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp Tyr Pro Glu

325

330

335

cat gtg acg gag tac ggc gtg cac tgg aat ttc ttc ttc acc ctc gca 1221

His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Ala

340

345

350

355

ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg cag tgg ctt 1269

Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr Gln Trp Leu

360

365

370

cgc tgg agt gtg ctt ggg gta atc atc tct ttg ctg cat cag ctg tgg 1317

Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His Gln Leu Trp

375

380

385

tta aca tat tat ctc caa tcc atc gtc ttc tca ttc ggc cgg tca ggt 1365

Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly Arg Ser Gly

390

395

400

atc ttt cta gca aac aag gaa ggc ttc tcc tct ctt cct ggt tat ctt 1413

Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro Gly Tyr Leu

405

410

415

tcc ata ttt ttg atc ggc ttg tct att gga gat cat gtt tta agg ctc 1461

Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val Leu Arg Leu

420

425

430

435

agt tta cca cca aga aga gag agg gtc gtg tca gaa aca aat gaa gag 1509

Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr Asn Glu Glu

440

445

450

cat gag cag agt cat ttt gag aga aaa aaa ttg gat ttg att atg gag 1557

His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu Ile Met Glu

455

460

465

ttg att gga tat agc tta ggc tgg tgg gca ctc tta gga ggc tgg att 1605

Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly Gly Trp Ile

470

475

480

tgg gcc ggc ggg gag gta tcc agg cgt tta gtaagtggac atctttggta 1655

Trp Ala Gly Gly Glu Val Ser Arg Arg Leu

485

490

atattgtacc tatactaatac cctgcataaa g gcc aac gct cct tat gta ttt 1707

59 / 72

Ala Asn Ala Pro Tyr Val Phe

495

500

tgg gta gcg gca tac aat acc acc ttt ctc ctc ggc tac ctc ctc ctt 1755

Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly Tyr Leu Leu Leu

505

510

515

acc cac att att cca tct ccc acc tct tcc caa aca tca cca tcg atc 1803

Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr Ser Pro Ser Ile

520

525

530

tta gtg cct ccc ttg ctc gac gct atg aat aaa aac ggt ctc gcg ata 1851

Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn Gly Leu Ala Ile

535

540

545

ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat gtg agc atg aag 1899

Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn Val Ser Met Lys

550

555

560

aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg tta atg ttg tat 1947

Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val Leu Met Leu Tyr

565

570

575

580

acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa gga cgg agg atc 1995

Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys Gly Arg Arg Ile

585

590

595

aag ata tagttaaagt gtttaccatg caggatactg agtatctcgg ttca

2045

Lys Ile

<210> 13

<211> 1797

<212> DNA

<213> *Cryptococcus neoformans*

<220>

<221> CDS

<222> (1)..(1794)

<400> 13

atg ggg gat tac aag tcg gcc aaa gag gcc ttt gtc tcg gat aac cca 48

Met Gly Asp Tyr Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro

1

5

10

15

ggt gct tct atc tgg agt atc aac gct gtc agc ctg gtc gca ctg gcg 96

Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala

20

25

30

aca tat gct ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc 144

Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu

35

40

45

ctg aac aac tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc 192

Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr

50

55

60

atc ttc tca act tcg cct ctc gta ttt acc tct ttt ttg tcc att att 240

Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile

65

70

75

80

tcc ctc gct ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt 288

Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser

85

90

95

tcg ccc gaa aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat 336

Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp

100

105

110

gag gaa cca gcg gaa cct gct tct gca gct gga tct gca gca gtc tca 384

Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser

115

120

125

cca gta aag ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta 432

Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu

130

135

140

6 2 / 7 2

tta tct ccc gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca 480

Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser

145 150 155 160

gct tca gga cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg 528

Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg

165 170 175

agg tcg cta tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac 576

Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp

180 185 190

tcc aag gtc aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct 624

Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser

195 200 205

agg gca acg aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt 672

Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe

210 215 220

ttg aca gtg tac cga gcg cac atg atg ctc atg act gtt atc tgc atc 720

Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile

225 230 235 240

ttg gcg gta gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa 768

Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu

6 3 / 7 2

245

250

255

gat ttt ggt act agt ctg atg gac gtg ggt gtc ggg tca ttc gtc ttt 816

Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe

260

265

270

tcc ctc ggt ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act 864

Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr

275

280

285

cct acg ccc tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc 912

Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr

290

295

300

cgc tcc ccg ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc 960

Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro

305

310

315

320

atc ctc gtc ctc ggc ttt ata cgg ttg att atg gtc aag gga tct gat 1008

Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp

325

330

335

tat cct gag cat gtg acg gag tac ggc gtg cac tgg aat ttc ttc ttc 1056

Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe

340

345

350

acc ctc gca ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg 1104

Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr

355

360

365

cag tgg ctt cgc tgg agt gtg ctt ggg gta atc atc tct ttg ctg cat 1152

Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His

370

375

380

cag ctg tgg tta aca tat tat ctc caa tcc atc gtc ttc tca ttc ggc 1200

Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly

385

390

395

400

cgg tca ggt atc ttt cta gca aac aag gaa ggc ttc tcc tct ctt cct 1248

Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro

405

410

415

ggt tat ctt tcc ata ttt ttg atc ggc ttg tct att gga gat cat gtt 1296

Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val

420

425

430

tta agg ctc agt tta cca cca aga aga gag agg gtc gtg tca gaa aca 1344

Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr

435

440

445

aat gaa gag cat gag cag agt cat ttt gag aga aaa aaa ttg gat ttg 1392

Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu



6 5 / 7 2

450

455

460

att atg gag ttg att gga tat agc tta ggc tgg tgg gca ctc tta gga 1440

Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly

465

470

475

480

ggc tgg att tgg gcc ggc ggg gag gta tcc agg cgt tta gcc aac gct 1488

Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala

485

490

495

cct tat gta ttt tgg gta gcg gca tac aat acc acc ttt ctc ctc ggc 1536

Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly

500

505

510

tac ctc ctc ctt acc cac att att cca tct ccc acc tct tcc caa aca 1584

Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr

515

520

525

tca cca tcg atc tta gtg cct ccc ttg ctc gac gct atg aat aaa aac 1632

Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn

530

535

540

ggt ctc gcg ata ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat 1680

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn

545

550

555

560

6 6 / 7 2

gtg agc atg aag aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg 1728

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val

565

570

575

tta atg ttg tat acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa 1776

Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys

580

585

590

gga cgg agg atc aag ata tag

1797

Gly Arg Arg Ile Lys Ile

595

<210> 14

<211> 598

<212> PRT

<213> Cryptococcus neoformans

<400> 14

Met Gly Asp Tyr Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro

1

5

10

15

Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala

20

25

30

Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu

6 7 / 7 2

35

40

45

Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr

50

55

60

Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile

65

70

75

80

Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser

85

90

95

Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp

100

105

110

Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser

115

120

125

Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu

130

135

140

Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser

145

150

155

160

Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg

165

170

175

6 8 / 7 2

Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp

180

185

190

Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser

195

200

205

Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe

210

215

220

Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile

225

230

235

240

Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu

245

250

255

Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe

260

265

270

Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr

275

280

285

Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr

290

295

300

Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro

305

310

315

320

69 / 72

Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp

325

330

335

Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe

340

345

350

Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr

355

360

365

Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His

370

375

380

Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly

385

390

395

400

Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro

405

410

415

Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val

420

425

430

Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr

435

440

445

Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu

7 0 / 7 2

450

455

460

Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly

465

470

475

480

Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala

485

490

495

Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly

500

505

510

Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr

515

520

525

Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn

530

535

540

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn

545

550

555

560

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val

565

570

575

Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys

580

585

590

Gly Arg Arg Ile Lys Ile

595

<210> 15

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 15

ggaattcatg tcgactttaa aacagagaaa agagg

35

<210> 16

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

7 2 / 7 2

<400> 16

gcatcgattt atagcttaat gaatattctt tttct atac

34

<210> 17

<211> 60

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 17

atggcaacag tacatcagga gaatatgtcg actttaaaac cggatccccg tcgtttaaac 60

<210> 18

<211> 60

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 18

ttatagctta atgaatattc tttttctata caagaaaacc gaattcgagc tcgtttaaac 60